RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _08/922,240_
Source: _1FWJ16_
Date Processed by STIC: _7/23/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY** or,
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u>
<u>VERSION 4.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> **http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
<u>Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:</u>

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby,
   Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 08/922,240

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3. ____Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length
Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading).
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa
"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFW16

RAW SEQUENCE LISTING   DATE: 07/23/2004
PATENT APPLICATION: US/08/922,240 TIME: 13:24:42

Input Set : A:\APBI-P01-007.TXT
Output Set: N:\CRF4\07232004\H922240.raw

```
     4 <110> APPLICANT: Schreiber, Stuart L.
     5        Belshaw, Peter
     6        Crabtree, Gerald R.
     8 <120> TITLE OF INVENTION: GENE THERAPY BY CELL SPECIFIC TARGETING
    11 <130> FILE REFERENCE: APBI-P01-007
    13 <140> CURRENT APPLICATION NUMBER: US 08/922,240
    14 <141> CURRENT FILING DATE: 1997-08-27
    16 <150> PRIOR APPLICATION NUMBER: US 60/024,666
    17 <151> PRIOR FILING DATE: 1996-08-27
    19 <160> NUMBER OF SEQ ID NOS: 3
    21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
    23 <210> SEQ ID NO: 1
    24 <211> LENGTH: 10
    25 <212> TYPE: PRT
    26 <213> ORGANISM: Unknown
    28 <220> FEATURE:
    29 <223> OTHER INFORMATION: Peptide
W--> 31 <221> NAME/KEY: VARIANT
    32 <222> LOCATION: 1
    33 <223> OTHER INFORMATION: Xaa = Abu: alpha-aminobutyric acid
W--> 35 <221> VARIANT
    36 <222> LOCATION: 2
    37 <223> OTHER INFORMATION: Xaa = Sar: sarcosine
W--> 39 <221> VARIANT
    40 <222> LOCATION: 3, 5, 8, 9
    41 <223> OTHER INFORMATION: Xaa = MeLeu: N-methylleucine
W--> 43 <221> VARIANT
    44 <222> LOCATION: 7
    45 <223> OTHER INFORMATION: Xaa = D-Ala: D-alanine
W--> 47 <221> VARIANT
    48 <222> LOCATION: 10
    49 <223> OTHER INFORMATION: Xaa = Ac-N-MeValinol ester
W--> 51 <400> 1
W--> 52 Xaa Xaa Xaa Val Xaa Ala Xaa Xaa Xaa Xaa
    53 1               5                 10
    56 <210> SEQ ID NO: 2
    57 <211> LENGTH: 12
    58 <212> TYPE: PRT
    59 <213> ORGANISM: Unknown
    61 <220> FEATURE:
    62 <223> OTHER INFORMATION: Peptide
W--> 64 <221> NAME/KEY: VARIANT
    65 <222> LOCATION: 1
```

[Handwritten annotations:] pp 1-3

Understood - please attempt to give source of genetic material as explanation for <213> Unknown (see item 11 on Error Summary Sheet)

Understood- (but insufficient)

same error

RAW SEQUENCE LISTING   DATE: 07/23/2004
PATENT APPLICATION: US/08/922,240   TIME: 13:24:42

Input Set : A:\APBI-P01-007.TXT
Output Set: N:\CRF4\07232004\H922240.raw

```
       66 <223> OTHER INFORMATION: Xaa = Fmoc-CpSar:
       67       9-fluorenylmethoxycarbonyl-cyclopentyl sarcosine
W--> 69 <221> VARIANT
       70 <222> LOCATION: 2
       71 <223> OTHER INFORMATION: Xaa = MeBmt:
       72       (4R)-N-methyl-4-butenyl-4-methyl-L-threonine
W--> 74 <221> VARIANT
       75 <222> LOCATION: 3
       76 <223> OTHER INFORMATION: Xaa = Abu: alpha-aminobutyric acid
W--> 78 <221> VARIANT
       79 <222> LOCATION: 4
       80 <223> OTHER INFORMATION: Xaa = Sar: sarcosine
W--> 82 <221> VARIANT
       83 <222> LOCATION: 5, 7, 10, 11
       84 <223> OTHER INFORMATION: Xaa = MeLeu: N-methylleucine
W--> 86 <221> VARIANT
       87 <222> LOCATION: (9)...(9)
       88 <223> OTHER INFORMATION: Xaa = D-Ala: D-alanine
W--> 90 <221> VARIANT
       91 <222> LOCATION: (12)...(12)
       92 <223> OTHER INFORMATION: Xaa = Valinol ester
W--> 94 <400> 2
W--> 95 Xaa Xaa Xaa Xaa Xaa Val Xaa Ala Xaa Xaa Xaa Xaa
       96  1                5                10
       99 <210> SEQ ID NO: 3
      100 <211> LENGTH: 11
      101 <212> TYPE: PRT
      102 <213> ORGANISM: Unknown
      104 <220> FEATURE:
      105 <223> OTHER INFORMATION: Peptide
W--> 107 <221> NAME/KEY: VARIANT
      108 <222> LOCATION: 1
      109 <223> OTHER INFORMATION: Xaa = Me-CpSar: methyl-cyclopentyl sarcosine
W--> 111 <221> VARIANT
      112 <222> LOCATION: 2
      113 <223> OTHER INFORMATION: Xaa = MeBmt:
      114       (4R)-N-methyl-4-butenyl-4-methyl-L-threonine
W--> 116 <221> VARIANT
      117 <222> LOCATION: 3
      118 <223> OTHER INFORMATION: Xaa = Abu: alpha-aminobutyric acid
W--> 120 <221> VARIANT
      121 <222> LOCATION: 4
      122 <223> OTHER INFORMATION: Xaa = Sar: sarcosine
W--> 124 <221> VARIANT
      125 <222> LOCATION: 5, 7, 10
      126 <223> OTHER INFORMATION: Xaa = MeLeu: N-methylleucine
W--> 128 <221> VARIANT
      129 <222> LOCATION: (11)...(11)
      130 <223> OTHER INFORMATION: Xaa = MeLeu-(OH): hydroxyl-N-methylleucine
```

what about Xaa at location 9? (see p.3)

RAW SEQUENCE LISTING   DATE: 07/23/2004
PATENT APPLICATION: US/08/922,240   TIME: 13:24:42

Input Set : **A:\APBI-P01-007.TXT**
Output Set: **N:\CRF4\07232004\H922240.raw**

```
W--> 132 <400> 3
W--> 133 Xaa Xaa Xaa Xaa Xaa Val Xaa Ala Xaa Xaa Xaa
     134 1               5               10
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/23/2004
PATENT APPLICATION: US/08/922,240   TIME: 13:24:43

Input Set : A:\APBI-P01-007.TXT
Output Set: N:\CRF4\07232004\H922240.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 1,2,3,5,7,8,9,10
Seq#:2; Xaa Pos. 1,2,3,4,5,7,8,10,11,12
Seq#:3; Xaa Pos. 1,2,3,4,5,7,9,10,11

VERIFICATION SUMMARY   DATE: 07/23/2004
PATENT APPLICATION: **US/08/922,240**   TIME: 13:24:43

Input Set : **A:\APBI-P01-007.TXT**
Output Set: **N:\CRF4\07232004\H922240.raw**

```
L:31 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:35 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:43 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:51 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:64 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:69 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:74 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:78 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:82 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:86 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:94 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:107 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:111 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:116 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:120 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:124 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:128 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:132 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
```